

FIGURE 1

mAb	Mean Fluorescence Intensity		% Gated	
	L1.2-CCR5	PBMC	L1.2-CCR5	PBMC
mouse IgG1	10	4	1	1
2D7	75	29	92	36
PA8	48	9	73	3
PA9	79	5	96	3
PA10	80	8	96	5
PA11	107	8	96	10
PA12	115	8	96	8
PA14	81	14	96	22

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FIGURE 2

INHIBITOR COMBINATION	CONCENTRATION RATIO	ASSAY	COMBINATION INDEX	
			90% Inhibition	50% Inhibition
PA12:2D7	10:1	Entry	0.043	0.291
	2:1	Fusion	0.017	0.019
	10:1	Fusion	0.087	0.067
	50:1	Fusion	0.158	0.046
PA12:PA14	10:1	Entry	0.437	0.535
	10:1	Fusion	0.22	0.263
PA14:2D7	1:1	Entry	2.85	1.85
	1:1	Fusion	1.34	1.74
PA12:PA11	1:1	Entry	0.707	0.641
PA12:RANTES	1000:1	Fusion	0.331	0.156
PA14:RANTES	100:1	Fusion	1.6	1.37
2D7:RANTES	100:1	Fusion	0.972	0.962
PA12:CD4-IgG2	10:1	Fusion	0.3	0.31
PA14:CD4-IgG2	1:1	Fusion	0.957	0.566
2D7:CD4-IgG2	1:1	Fusion	1.127	0.302

FIGURE 3

	Epitopes	IC ₅₀ values (μg/ml)			
		cell-cell fusion inhibition	viral entry inhibition	gp120-binding inhibition	calcium flux inhibition
PA8	Nt	-	-	-	-
PA9	Nt/ECL2	-	-	0.24	-
PA10	Nt/ECL2	-	-	0.13	-
PA11	Nt	25.5	-	0.33	-
PA12	Nt	10.0	-	0.24	-
PA14	Nt/ECL2	1.7	.024	1.58	6.4
2D7	ECL2	1.6	.026	1.38	45

FIGURE 4

	1	5	10	15	20	25	30
M D Y Q V S S P I Y D I N Y V T S E P C Q K I N K Q I A A R	92 54 90 nd 83 63 82 nd 46 40 40 90 90 86 111 49 37 45 44 37 52 27 92 65	118 63 78 nd 52 36 32 nd 4 2 0 53 7 45 100 47 32 36 44 37 34 24 134 36	16 13 0 nd 113 9 13 nd 10 0 19 62 52 29 71 36 32 36 45 30 55 18 145 40	21 14 0 nd 115 39 22 nd 14 8 15 101 48 99 94 27 97 45 45 39 53 13 113 46	70 32 0 nd 112 80 81 nd 40 22 51 74 70 46 85 32 47 36 48 40 47 22 144 64	68 30 0 nd 76 81 51 nd 34 12 49 76 68 40 86 30 41 49 46 34 54 12 93 43	9 86 75 nd 85 88 89 nd 57 40 64 78 84 66 76 80 71 44 86 64 76 46 99 23
2D7							
PA8							
PA9							
PA10							
PA11							
PA12							
PA14							

2

	90					95					100				
	H	Y	A	A	A	Q	W	D	F	G	N	T	M	C	Q
2D7	70	89				40	130	40	66		38	72	82	0	74
PA8	38	92				49	118	32	115		96	86	68	10	39
PA9	31	66				27	81	16	159		118	89	57	0	43
PA10	67	83				36	139	18	133		112	97	61	0	40
PA11	39	81				38	91	25	78		60	94	71	10	60
PA12	63	67				35	91	29	77		76	79	102	25	55
PA14	71	79				63	83	23	86		47	89	80	8	77

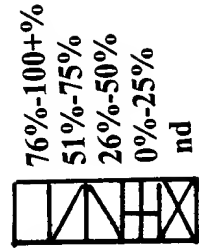
ECL1

	170										175										180										185										190									
	R	S	Q	K	E	G	L	H	Y	T	C	S	S	H	F	P	Y	S	Q	Y	Q	F	W	K	N	F	Q																							
2D7	62	55	17	0	0	62	64	65	0	83	95	51	52	32	32	80	92	71	42	34	71	39	33	45	102																									
PA8	38	40	58	31	0	65	43	61	26	90	100	51	41	46	90	68	74	59	38	95	33	40	27	62																										
PA9	39	28	63	15	0	34	73	0	29	93	112	27	43	27	79	63	75	74	13	51	38	72	35	59																										
PA10	45	59	34	19	0	30	21	0	25	84	96	32	61	39	77	82	51	68	16	39	45	16	38	70																										
PA11	67	58	45	33	0	49	118	130	37	78	95	40	48	38	91	99	81	34	44	71	47	23	50	92																										
PA12	52	56	36	31	0	52	102	136	59	73	85	44	49	42	101	90	45	56	33	66	37	28	51	74																										
PA14	1	85	88	59	0	80	74	72	9	109	83	52	64	50	40	93	88	65	34	79	55	51	72	71																										

ECL2

	265												270												275																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
	Q	E	F	F	G	L	N	N	C	S	S	S	S	S	N	R	L	D	Q																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						

ECL3



	1	5	10	15	20	25	30																							
	M	D	Y	Q	V	S	S	P	I	Y	D	I	N	Y	T	S	E	P	C	Q	K	I	N	K	Q	I	A	A	R	
2D7			92	90	nd	83	82	nd	40	90	80	88	111	40	88	111	40	88	111	40	88	111	40	88	111	40	88	111	40	88
PA8			118	78	nd	52	22	nd	4	2	0	19	62	2	45	100	47	52	50	41	57	54	24	134	134	134	134	134	134	
PA9			16	13	0	nd	213	19	13	nd	10	10	19	62	52	73	63	63	39	45	30	53	18	145	145	145	145	145	145	
PA10			21	14	0	nd	175	33	22	nd	14	8	15	101	49	94	97	47	45	45	30	53	13	133	133	133	133	133	133	
PA11			30	34	0	nd	112	80	81	nd	40	22	37	79	49	85	57	49	56	44	40	46	22	146	146	146	146	146	146	
PA12			38	39	0	nd	76	81	51	nd	34	12	49	76	40	88	46	51	49	49	49	52	12	93	93	93	93	93	93	
PA14			9	86	75	nd	85	88	89	nd	57	40	63	78	84	76	80	79	88	88	88	78	98	98	98	98	98	98	98	

IN

	H	Y	A	A	A	Q	W	D	F	G	N	T	M	C	Q
2D7	70	89				45	130	40	60		55	72	82	0	72
PA8	85	92				49	118	52	115		96	86	53	10	49
PA9	55	61				27	81	16	159		138	89	57	0	43
PA10	57	83				35	139	18	133		112	87	53	0	40
PA11	55	81				38	91	25	78		96	94	77	10	46
PA12	65	87				35	91	48	77		78	79	102	25	35
PA14	72	78				62	83	23	88		43	89	80	8	67

ECL 1

	170				175				180				185				190									
	R	S	Q	K	E	G	L	H	Y	T	C	S	H	F	P	Y	S	Q	Y	Q	F	W	K	N	F	Q
2D7	52	55	17	0							7	83	95	53	52	52	80	92	72	49	24	39	54	54	102	
PA8	36	46	59	59							96	90	100	41	41	90	98	74	39	38	95	34	6	5	52	
PA9	38	21	35	15							25	83	112	57	45	78	95	75	73	13	51	58	12	54	53	
PA10	16	59	51	19							0	84	98	3	51	77	82	35	32	16	39	45	16	35	78	
PA11	29	52	45								130	78	95	48	48	91	99	91	53	24	74	37	23	46	92	
PA12	52	55	55								136	73	85	46	46	101	90	35	33	23	46	37	20	35	75	
PA14	11	85	88								9	109	83	57	37	100	83	88	46	39	78	36	6	74	74	

ECL 2

[illegible]

ECL 3

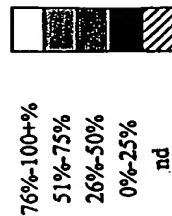
[illegible]

FIGURE 5A

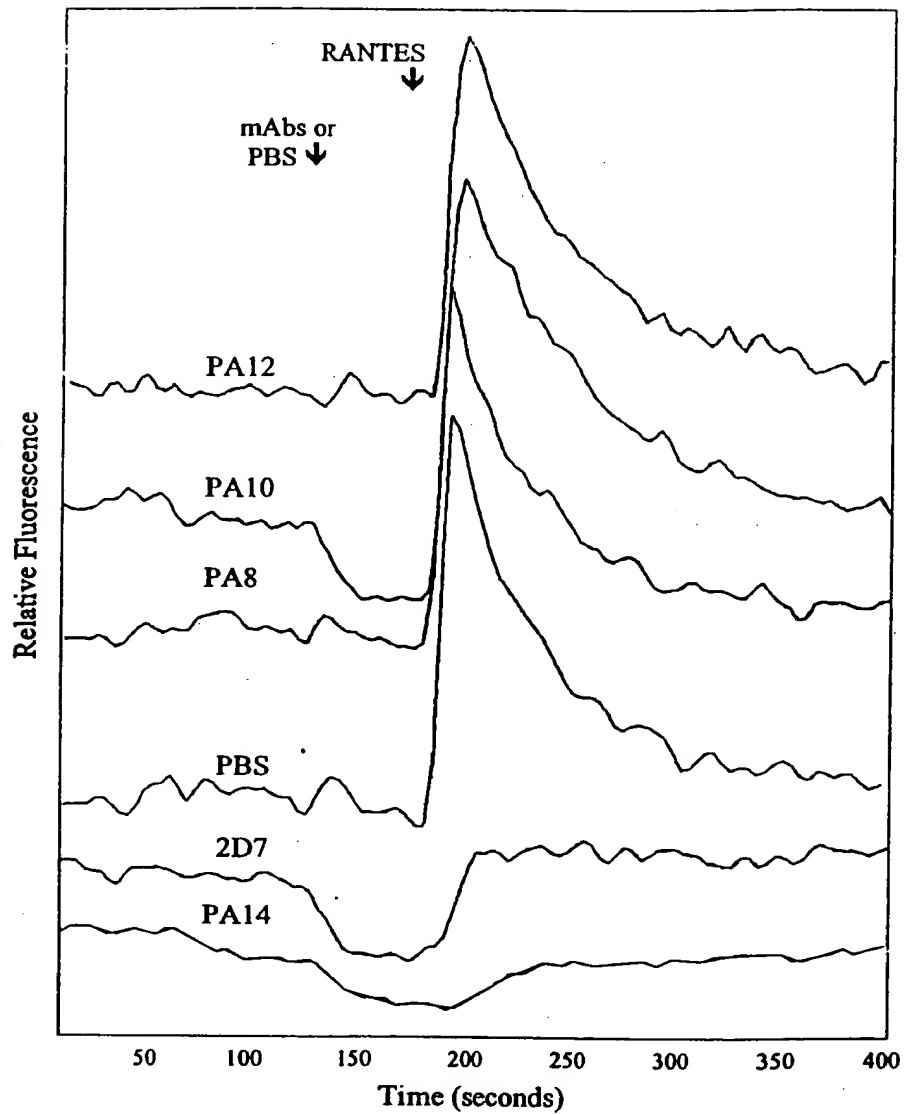
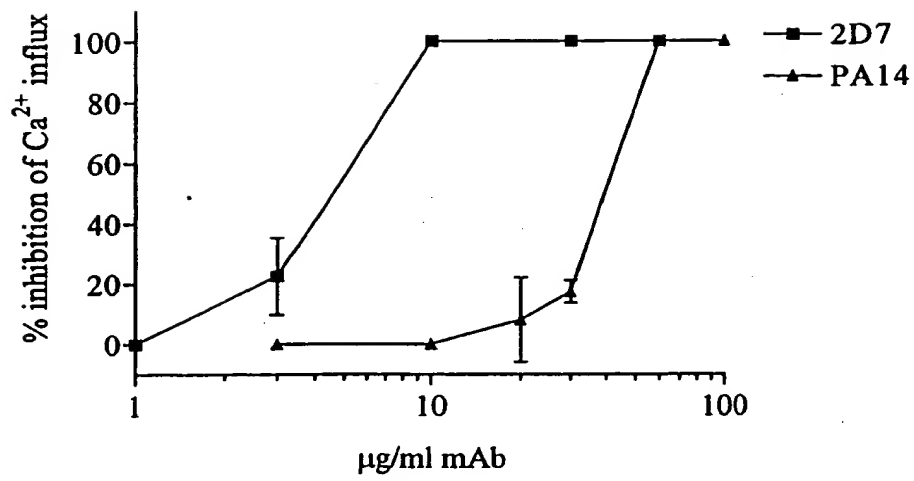
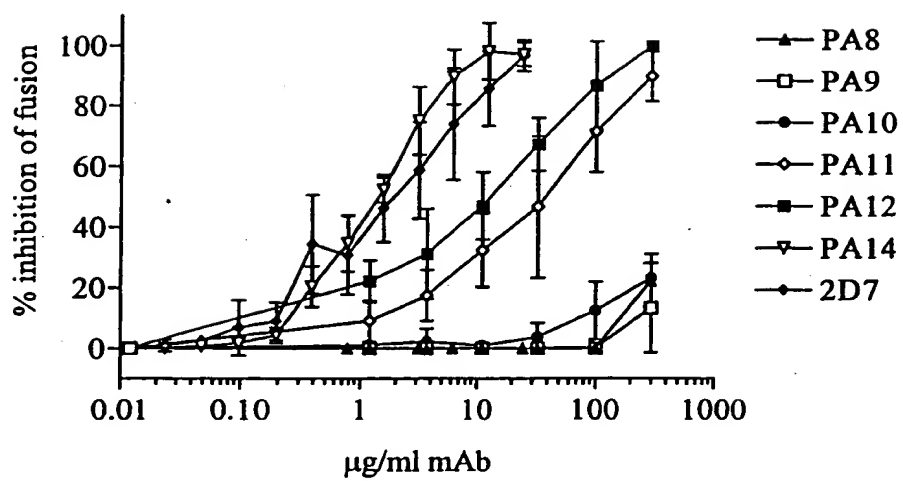


FIGURE 5B



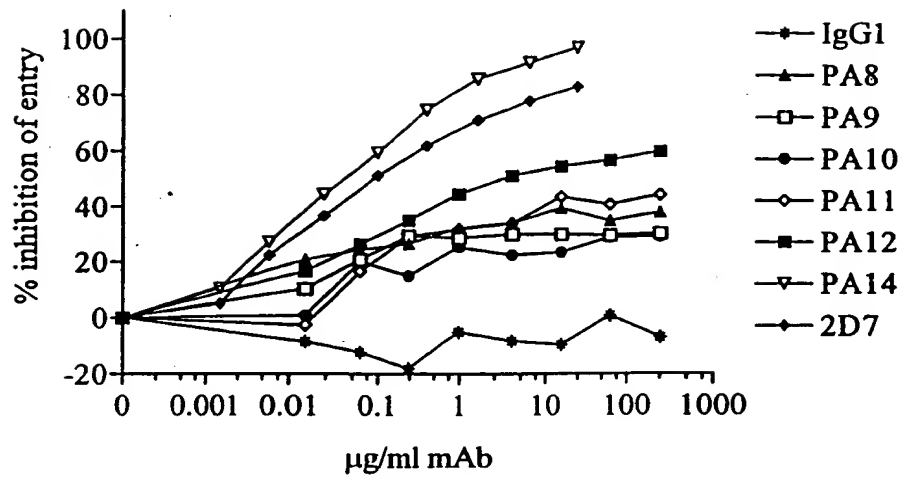
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FIGURE 6A



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FIGURE 6B



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FIGURE 6C

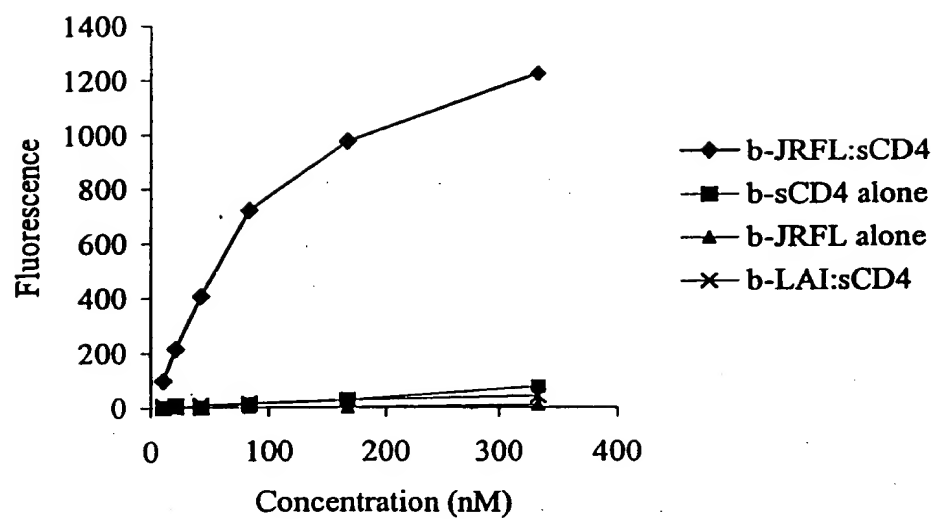


FIGURE 6D

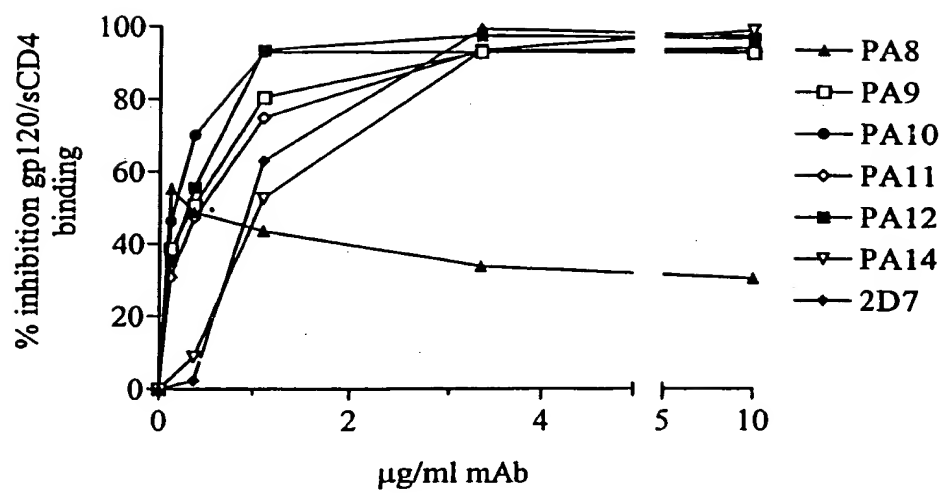


FIGURE 7

